

Applicant(s)

Van Ommen, et al.

Examiner:

C. Wilder

Serial No.:

09/445,174

Group Art Unit:

1655

TECH CENTER 1600/2900

Filed:

April 24, 2000

Docket:

294-78

OCT 30 2000

For:

DIAGNOSTIC TEST KIT FOR

Dated:

October 18, 2000

TECH CENTER 16:0/2000

DETERMINING A

PREDISPOSITION FOR **BREAST AND OVARIAN** CANCER, MATERIALS AND

METHODS FOR SUCH **DETERMINATION**

Assistant Commissioner for Patents Washington, DC 20231

I hereby certify this correspondence is being deposited with the United States Postal Service as first class mail, postpaid in an envelope, addressed to:

Assistant Commissioner for Patents, Washington, D.C.

20231 on October 18, 2000

Dated: 10/18/00 \

RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATION CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Sir:

In response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures mailed September 8, 2000, Applicants enclose herewith the following:

- Diskette containing a substitute Sequence Listing in computer-readable form, 1. corrected as directed in the Notice;
 - A substitute paper copy of the "Sequence Listing"; and 2.

3. A copy of the Notice to Comply.

REMARKS

Applicants have amended the Sequence Listing to conform with the above-referenced Notice to Comply. Entry of the amended Sequence Listing into the specification of the application is respectfully requested.

The Notice to Comply dated September 8, 2000 indicates that the due date for a response to the Notice is the one-month shortened statutory period. This Response is filed within the second month after the September 8, 2000 communication. Accordingly, a Petition for a One Month Extension of Time and the appropriate fee are filed concurrently herewith.

The assignee is a small entity. Therefore, the reduced extension of time fee is being paid. A Declaration Claiming Small Entity is enclosed.

In compliance with the sequence rules as required under 37 C.F.R. §§1.821-1.825, Applicants have amended SEQ. ID NO.: 21 to delete reference to "n". The presence of "n" in the sequence listing was an error. Applicants provide herewith a computer readable form and a paper copy of the corrected Sequence Listing thereby satisfying the requirement under 37 C.F.R. §§1.821 et seq.

Under 37 C.F.R. 1.821(f), the Applicants' attorney hereby states that the contents of the computer readable form and the paper copy are the same. Under 37 C.F.R. §1.821(g), the

Applicants' attorney also states that the inclusion of this Sequence Listing does not include any new matter. Accordingly, it is respectfully requested that the Sequence Listing be entered into the application.

If the Examiner has any questions relating to this Amendment or to this application in general, it is respectfully requested that the Examiner contact the Applicants' undersigned attorney at the telephone number provided below.

Respectfully submitted,

ames F. Harrington

Registration No. 44,741

Attorney for Applicants

HOFMANN & BARON, LLP 6900 Jericho Turnpike Syosset, New York 11791 (516) 822-3550 JFH:jlw

121195_1.DOC



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST	NAMED APPLICANT	АТ	TORNEY DOCKET NO.
T			1	E	XR.
			Debra Shoe	maker	
			ART U	VIT	PAPER NUMBER
L			J DATE MAI	LED:	

Please find below a communication from the EXR. in charge of this application

Commissioner of Patents

1. The communication filed 7/13/2000 is not fully responsive to the Office communication mailed 6/13/2000 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the above-mentioned reply appears to be *bona fide* attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

2. Any inquiry concerning this communication or earlier communications from the Exr. Should be directed to Cynthia Wilder whose telephone number is (703) 305-1680. The Exr. Can normally be reached on Monday-Thursday from 6:30-5:00 pm (Eastern Time).

If attempts to reach the Exr. by telephone are unsuccessful, the Exr.'s supervisor Gary Jones, can be reached at (703) 308-1152. The official fax number for group 1600 is (703) 308-4242, unofficial fax number for group 1600 is (703) 308-8724.

Any inquiry of a general nature or relating to the status of the application should be directed to the groups receptionist whose telephone number is (703) 308-0196.

Jelio

Cynthia Walder

Cynthia B. Wilder, PhD September 5, 2000

S. Flomer

Application No.: 9/445, 174

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s)

	A	 This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
		 This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
		3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
		4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
/	X	5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
		6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
		7. Other:
	Ap	plicant Must Provide:
	A	An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
		An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entrinto the specification.
•	A	A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).
	_	ti and and in a compliance to these requirements, please contact:

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For Patentin software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

BRRORERED (O)



The Biotechnology Systems Branch of the Scientific and Rechnical Information Center (SIIC) itelected errors when processing the following computer readable form

Application Serial Number 201/19

Date Processed by STIC

THE ATTACHED PRINTOUT EXPLAINS DETECTED FRRORS

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT. WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER 703-308-4212

TO REDUCE ERRORED SEQUENCE EISTINGS PLEASE USE THE CHECKER VERSION 3.0 PROGRAM ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK:OFFICE WEBSITE SEE BELOW

Checker Version 3.0

The Checker Version 3.0 application is a state-of the art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence li egenerated for the original version of \$7.0 CR \$51821=1825 effective October 418 990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual). Property Organization (WIPO) Standard ST25

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USP/10).

Use of Checker prior to filing the sequence listing is expected for esult in rewer errored sequence listings, thus saying time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checkera

医动能器性动物的运费 计

	ERROR DETECTED	SUGGESTED CORRECTION SERIA	L NUMBER:	
ATTAL	NEW DITLES CASES: PI	EASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WI	ERE INSERTED BY PTO SOFTW	ARE
1	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the nex This may occur if your file was retrieved in a word processor after. Please adjust your right margin to .3, as this will prevent "wrappin	d line. creating it.	RECEIVED
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " do		AUG 16 2000
	Astables Williams	This may occur if your file was retrieved in a word processor after Please adjust your right margin to .3, as this will prevent "wrapping to .3, as the will prevent will be will prevent will be wrapping to .3, as the will prevent will be wrapping to .3, as the wrapping to .3, as the will be wrapp	creating it.	ĘCH CENTER 1600/2900
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length.	his includes spaces.	
4	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may between the numbering. It is recommended to delete any tabs and		3
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Southease ensure your subsequent submission is saved in ASCII text.		
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more to As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having varianticate in the (ix) feature section that some may be missing.	e.	
7	Patentin ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> sec sequence(s) Normally, PatentIn would automatic previously coded nucleic acid sequence. Please manually copy to the subsequent amino acid sequence. This applies primaril sections for Artificial or Unknown sequences.	cally generate this section from the the relevant <220>-<223> section	
8	Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please use the followin (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not Insert any headin (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped	gs under "SEQUENCE CHARACT	TERISTICS")
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" respo		
9	_ Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please use the followin <210> sequence id number <400> sequence id number 000	g format for each skipped sequenc	e.
10	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Lis Use of <220> to <223> is MANDATORY if n's or Xaa's are pres In <220> to <223> section, please explain location of n or Xaa,	ent.	ents.
11	Use of <213>Organism (NEW RULES)	Sequence(s) are missing this mandatory field or its res	ponse.	-
12	_ Use of <220>Feature (NEW RULES)	Sequence(s) are missing the <220>Feature and associate Use of <220> to <223> is MANDATORY if <213>ORGANISM Please explain source of genetic material in <220> to <223 (See "Federal Register," 6/01/98, Vol. 63, No. 10	is "Ártificial" or "Unknown" > section.	23 of new Rules)
13	_ Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin versifile, resulting in missing mandatory numeric identifiers and respinstead, please use "File Manager" or any other means to copy	onses (as indicated on raw sequen	ce listing).

RAW SEQUENCE LISTING DATE: 07/26/2000 PATENT APPLICATION: US/09/445,174 TIME: 10:17:06

Input Set : A:\115541_1.txt

Output Set: N:\CRF3\07262000\I445174.raw

Couected Diskette Needed

```
1 <110> APPLICANT: van Ommen, Garrit J.B.
        Petrij-Bosch, Anne
        Bakker, Egbert
                                                                            See P. 5
        Devilee, Peter
  <120> TITLE OF INVENTION: A diagnostic test kit for determining a predisposition
        for breast and ovarian cancer, materials and methods
        for such determination
11 <130> FILE REFERENCE: P22163CA00
13 <140> CURRENT APPLICATION NUMBER: US 09/445,174
14 <141> CURRENT FILING DATE: 2000-04-24
16 <150> PRIOR APPLICATION NUMBER: PCT/NL98/00325
17 <151> PRIOR FILING DATE: 1998-06-03
19 <150> PRIOR APPLICATION NUMBER: EP 97201700.8
20 <151> PRIOR FILING DATE: 1997-06-04
22 <160> NUMBER OF SEQ ID NOS: 23
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
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35 <400> SEQUENCE: 1
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36 ctagcctggg caacaacga
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 20
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
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48 <400> SEQUENCE: 2
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52 <210> SEQ ID NO: 3
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54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
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                                                                     21
62 ggatggcctt ttagaaagtg g
65 <210> SEQ ID NO: 4
66 <211> LENGTH: 20
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
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>

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/445,174 DATE: 07/26/2000 TIME: 10:17:06

Input Set : A:\115541_1.txt
Output Set: N:\CRF3\07262000\1445174.raw

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80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
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84 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
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91 <210> SEQ ID NO: 6
92 <211> LENGTH: 20
93 <212> TYPE: DNA "
94 <213> ORGANISM: Artificial Sequence
96 <220> FEATURE:
97 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse >
         for D17S1323
98
100 <400> SEQUENCE: 6
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101 aagcaacttt gcaatgagtg
104 <210> SEQ ID NO: 7
105 <211> LENGTH: 22
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
          for first PCR
111
113 <400> SEQUENCE: 7
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 114 tcacagtgca gtgaattgga ag
 117 <210> SEQ ID NO: 8
 118 <211> LENGTH: 24
 119 <212> TYPE: DNA -
 120 <213> ORGANISM: Artificial Sequence ?
 122 <220> FEATURE:
 123 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
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 124
 126 <400> SEQUENCE: 8
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 127 gtagccagga cagtagaagg actg
 130 <210> SEQ ID NO: 9
 131 <211> LENGTH: 22
 132 <212> TYPE: DNA ^
 133 <213> ORGANISM: Artificial Sequence
 135 <220> FEATURE:
 136 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
 137
           for second PCR
 139 <400> SEQUENCE: 9
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RAW SEQUENCE LISTING DATE: 07/26/2000 PATENT APPLICATION: US/09/445,174 TIME: 10:17:06

Input Set : A:\115541_1.txt

Output Set: N:\CRF3\07262000\I445174.raw

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144 <211> LENGTH: 21
145 <212> TYPE: DNA .
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
         for second PCR
150
152 <400> SEQUENCE: 10
                                                                       21
153 ggccactttg taagctcatt c
156 <210> SEQ ID NO: 11
157 <211> LENGTH: 19
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
164 <400> SEQUENCE: 11
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165 aaccaccaag gtccaaagc
168 <210> SEQ ID NO: 12
169 <211> LENGTH: 24
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
176 <400> SEQUENCE: 12
177 gtagccagga cagtagaagg actg
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182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
 188 <400> SEQUENCE: 13
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 192 <210> SEQ ID NO: 14
 193 <211> LENGTH: 20
 194 <212> TYPE: DNA
 195 <213> ORGANISM: Artificial Sequence
 197 <220> FEATURE:
 198 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
 200 <400> SEQUENCE: 14
                                                                        20
 201 teccattgag aggtettget
 204 <210> SEQ ID NO: 15
 205 <211> LENGTH: 20
 206 <212> TYPE: DNA <
 207 <213> ORGANISM: Artificial Sequence
 209 <220> FEATURE:
 210 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
 212 <400> SEQUENCE: 15
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RAW SEQUENCE LISTING DATE: 07/26/2000 PATENT APPLICATION: US/09/445,174 TIME: 10:17:06

Input Set : A:\115541_1.txt

Output Set: N:\CRF3\07262000\I445174.raw

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219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
224 <400> SEQUENCE: 16
225 gaaaaaaaag tacaaccaaa tgcc
                                                                             24
228 <210> SEQ ID NO: 17
229 <211> LENGTH: 24
230 <212> TYPE: DNA 4
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
236 <400> SEQUENCE: 17
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240 <210> SEQ ID NO: 18
241 <211> LENGTH: 24
242 <212> TYPE: DNA /
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
248 <400> SEQUENCE: 18
                                                                             24
249 taccctataa gccagaatcc agaa
252 <210> SEQ ID NO: 19
253 <211> LENGTH: 21
 254 <212> TYPE: DNA
 255 <213> ORGANISM: Artificial Sequence
 257 <220> FEATURE:
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 260 <400> SEQUENCE: 19
 261 ggccactttg taagctcatt c
 264 <210> SEQ ID NO: 20
 265 <211> LENGTH: 720
 266 <212> TYPE: DNA
 267 <213> ORGANISM: Homo sapiens
 269 <220> FEATURE:
 270 <223> OTHER INFORMATION: /note="Exon 22 of BRCA1 and its flanking intron
           sequences, pos. 79441-80160"
 273 <400> SEQUENCE: 20
 274 agaggtottg ctataagcot toatooggag agtgtagggt agagggootg ggttaagtat 60
 275 gcagattact gcagtgattt tacatctaaa tgtccatttt agatcaactg gaatggatgg 120
276 tacagctgtg tggtgcttct gtggtgaagg agctttcatc attcaccctt ggcacagtaa 180
 277 gtattggtg ccctgtcaga gaggaggac acaatattct ctcctgtgag caagactggc 240
278 acctgtcagt ccctatggat gccctactg tagcctcaga agtcttctct gcccacatac 300
 279 ctgtgccaaa agactccatc tgtaagggat gggtaaggat ttgagaactg cacatattaa 360
 280 atatactgag ggaagacttt ttccctctaa ctctttttcc catatgtccc tccccctcct 420
 281 ctctgtgact gccccagcat actgtgtttc aacaaatcat caagaaatga tgggctggag 480
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RECEIVED

AUG 18 2000

LECH: CENTER 160012900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/445,174

DATE: 07/26/2000 TIME: 10:17:06

Input Set : A:\115541_1.txt

Output Set: N:\CRF3\07262000\I445174.raw

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282 gctgggcatg gtggctcatg tctgtaatcc cagcactttg ggaggccgag gcaggtggat 540
     283 cactigicag gagtitgaga ccagcotggo caacatggtg aaaccccato tgtactaaaa 600 284 aaaaaaaaac aaaaagtago caggootggt ggagcatgoo tgtaatgooa gotattiggg 660
     285 aagttgaggt gtgagcatcg cttgaacgtg ggaggcagag gttgcagtga gccaagattg 720
     288 <210> SEQ ID NO: 21
     289 <211> LENGTH: 180
     290 <212> TYPE: DNA /
     291 <213> ORGANISM: Homo sapiens
     293 <220> FEATURE:
     294 <223> OTHER INFORMATION: /note="Intronic region flanking exon 12, pos.
                 44423 - 44600"
      295
     297 <400> SEQUENCE: 21
W--> 298 cctgtaatcc cagcactttg ggaggccgag gcgggaggat catgtgfint caggagatcc 60 299 agaccatcct ggctaacacg gtgaaacacc atttctacta aaactacaaa aaattagctg 120
      300 ggcatggtgg cgggcgcctg taatcccagc tactcaggag gctgaagcag aagaatggct 180
      303 <210> SEQ ID NO: 22
      304 <211> LENGTH: 180
      305 <212> TYPE: DNA /
      306 <213> ORGANISM: Homo sapiens
      308 <220> FEATURE:
      309 <223> OTHER INFORMATION: /note="Intronic region flanking exon 13, pos.
                  48256 - 48436"
      310
      312 <400> SEQUENCE: 22
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      315 ggcgtggtgg cacatgcctg taatcccagc tacttgggag ctacggtgcc tggcctagtt 180
      318 <210> SEQ ID NO: 23
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      320 <212> TYPE: DNA
      321 <213> ORGANISM: Homo sapiens
      323 <220> FEATURE:
      324 <223> OTHER INFORMATION: /note="Deletion-function fragment"
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327 agaccatcet ggetaacacg gtgaaacacc atttctacta aaactacaaa aaattageeg 60

Mandatory 227 for few 1227 of 1227 for plain to residues

1221 plain to residues

122 plain to residues

128 plain to residues

128 plain to residues

129 plain to residues

120 plain to residues

120 plain to residues

121 plain to residues

122 plain to residues

122 plain to residues

123 plain to residues

125 plain to residues

125 plain to residues

127 plain to residues

128 plain

......

RECIENTER 1600/2800

326 <400> SEQUENCE: 23

VERIFICATION SUMMARY PATENT APPLICATION: US/09/445,174

DATE: 07/26/2000 TIME: 10:17:07

Input Set : A:\115541_1.txt
Output Set: N:\CRF3\07262000\1445174.raw

L:298 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21 L:298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21 L:298 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21

RECEIVED AUG 16 2000 TECH CENTER 1600/2900